

Dev

1641

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/308,435

DATE: 12/15/1999
TIME: 12:53:08

Input Set: I308435.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

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1  <110> APPLICANT: Astra Aktiebolag
2  <120> TITLE OF INVENTION: VACCINE DELIVERY SYSTEM AND METHOD OF PRODUCTION
3  <130> FILE REFERENCE: H1939-1 WO
4  <140> CURRENT APPLICATION NUMBER: US/09/308,435
5  <141> CURRENT FILING DATE: 1999-05-19
6  <150> EARLIER APPLICATION NUMBER: SE 9801288-3
7  <151> EARLIER FILING DATE: 1998-04-14
8  <160> NUMBER OF SEQ ID NOS: 4
9  <170> SOFTWARE: PatentIn Ver. 2.0
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11 <211> LENGTH: 1670
12 <212> TYPE: DNA
13 <213> ORGANISM: Helicobacter pylori
14 <220> FEATURE:
15 <221> NAME/KEY: CDS
16 <222> LOCATION: (793)..(1572)
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20   gatttgattt tagggaatta catgcaagt aatgaaaaaa acattcaagc gtttgcccc 180
21   aaacaataag gtaaaaaatg ccactcactc atttgaatga agaaaaatcaa cctaaaaatgg 240
22   tggatatagg ggataaagaa accactgaaa gaatcgctct agcaagcggc cgtatcagca 300
23   tgaataaaga ggcttatgac gctattatca atcatggcgt caaaaagggt ccggtattac 360
24   aaactgctat tattgctggg attatggggg ctaaaaagac aagcgaactc attcccatgt 420
25   gccatccaat catgctcaat ggggtggata ttgatatttt agaagaaaaa gagacttgta 480
26   gttttaaact ctatgcgaga gtcaaaactc aagctaaaac gggcgtagaa atggaagcgc 540
27   taatgagtgt gagcgtaggg cttttaacca tttatgacat ggtgaaagcc attgataaga 600
28   gcatgacaat tagcgtgtgt atgctggaat ataaaagtgg aggcaaaagt ggggattata 660
29   acgctaaaaa atagaaaaag actgataatc taaagatatt agggtaaaat aacattttga 720
30   caacaaaagc gtgttggttg cttcggattt gttgttatag aagtctaaaa tattacaatc 780
31   aaggatagaa cg atg aga gca aat aat cat ttt aaa gat ttt gca tgg aaa 831
32   Met Arg Ala Asn Asn His Phe Lys Asp Phe Ala Trp Lys
33   1 5 10
34   aaa tgc ctt tta ggc gcg agc gtg gtg gct tta tta gtg gga tgc agc 879
35   Lys Cys Leu Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Cys Ser
36   15 20 25
37   ccg cat att att gaa acc aat gaa gtc gct ttg aaa ttg aat tac cat 927
38   Pro His Ile Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His
39   30 35 40 45
40   cca gct agc gag aaa gtt caa gcg tta gat gaa aag att ttg ctt tta 975
41   Pro Ala Ser Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Leu
42   50 55 60
43   agg cca gct ttc caa tat agc gat aat atc gct aaa gag tat gaa aac 1023
44   Arg Pro Ala Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn

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48          80          85          90
49    caa ggc tat aag gtt att agc gta gat agc agc gat aaa gac gat ttt 1119
50    Gln Gly Tyr Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe
51          95          100          105
52    tct ttt gca caa aaa aaa gaa ggg tat ttg gcg gtt gct atg aat ggc 1167
53    Ser Phe Ala Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly
54    110          115          120          125
55    gaa att gtt tta cgc ccc gat cct aaa agg acc ata cag aaa aaa tca 1215
56    Glu Ile Val Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser
57          130          135          140
58    gaa ccc ggg tta tta ttc tcc acc ggt ttg gac aaa atg gaa ggg gtt 1263
59    Glu Pro Gly Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val
60          145          150          155
61    tta atc ccg gct ggg ttt att aag gtt acc ata cta gag cct atg agt 1311
62    Leu Ile Pro Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser
63          160          165          170
64    ggg gaa tct ttg gat tct ttt acg atg gat ttg agc gag ttg gac att 1359
65    Gly Glu Ser Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile
66          175          180          185
67    caa gaa aaa ttc tta aaa acc acc cat tca agc cat agc ggg ggg tta 1407
68    Gln Glu Lys Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu
69    190          195          200          205
70    gtt agc act atg gtt aag gga acg gat aat tct aat gac gcg atc aag 1455
71    Val Ser Thr Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys
72          210          215          220
73    agc gct ttg aat aag att ttt gca aat atc atg caa gaa ata gac aaa 1503
74    Ser Ala Leu Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys
75          225          230          235
76    aaa ctc act caa aag aat tta gaa tct tat caa aaa gac gcc aaa gaa 1551
77    Lys Leu Thr Gln Lys Asn Leu Glu Ser Tyr Gln Lys Asp Ala Lys Glu
78          240          245          250
79    tta aaa ggc aaa aga aac cga taaaaacaaa taacgcataa gaaaagaacg 1602
80    Leu Lys Gly Lys Arg Asn Arg
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92          20          25          30
93    Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser
94          35          40          45

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99      Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn Gln Gly Tyr
100                      85                      90                      95
101      Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe Ser Phe Ala
102                      100                      105                      110
103      Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly Glu Ile Val
104                      115                      120                      125
105      Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser Glu Pro Gly
106                      130                      135                      140
107      Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val Leu Ile Pro
108                      145                      150                      155                      160
109      Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser Gly Glu Ser
110                      165                      170                      175
111      Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile Gln Glu Lys
112                      180                      185                      190
113      Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu Val Ser Thr
114                      195                      200                      205
115      Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys Ser Ala Leu
116                      210                      215                      220
117      Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys Lys Leu Thr
118                      225                      230                      235                      240
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121      Lys Arg Asn Arg
122                      260

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123 <210> SEQ ID NO 3

124 <211> LENGTH: 1670

125 <212> TYPE: DNA

126 <213> ORGANISM: Helicobacter pylori

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129 <222> LOCATION: (793)..(1572)

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135      tggatatagg ggataaagaa accactgaaa gaatcgctct agcaagcggg cgtatcagca 300
136      tgaataaaga ggcttatgac gctattatca atcatggcgt caaaaagggg cgggtattac 360
137      aaactgctat tattgctggg attatggggg ctaaaaagac aagcgaactc attcccatgt 420
138      gccatccaat catgctcaat ggggtggata ttgatatttt agaagaaaaa gagacttgta 480
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143      caacaaaagc gtgttggttg cttcggattt gttgttatag aagtctaaaa tattacaatc 780
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148	Lys	Cys	Leu	Leu	Gly	Ala	Ser	Val	Val	Ala	Leu	Leu	Val	Gly
149		15				20				25				
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153	cca	gct	agc	gag	aaa	ggt	caa	gcg	tta	gat	gaa	aag	att	ttg
154	Pro	Ala	Ser	Glu	Lys	Val	Gln	Ala	Leu	Asp	Glu	Lys	Ile	Leu
155				50					55				60	
156	agg	cca	gct	ttc	caa	tat	agc	gat	aat	atc	gct	aaa	gag	tat
157	Arg	Pro	Ala	Phe	Gln	Tyr	Ser	Asp	Asn	Ile	Ala	Lys	Glu	Tyr
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169	Glu	Ile	Val	Leu	Arg	Pro	Asp	Pro	Lys	Arg	Thr	Ile	Gln	Lys
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176					160				165				170	
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178	Gly	Glu	Ser	Leu	Asp	Ser	Phe	Thr	Met	Asp	Leu	Ser	Glu	Leu
179				175					180				185	
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183	ggt	agc	act	atg	ggt	aag	gga	acg	gat	aat	tct	aat	gac	gcg
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192	tta	aaa	ggc	aaa	aga	aac	cga	taaaaa	caaaa	taacgcataa	gaaaagaacg			
193	Leu	Lys	Gly	Lys	Arg	Asn	Arg							
194				255					260					

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200 <213> ORGANISM: Helicobacter pylori
201 <400> SEQUENCE: 4
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210      Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn Lys Phe Lys
211      65          70          75          80
212      Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn Gln Gly Tyr
213      85          90          95
214      Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe Ser Phe Ala
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222      Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser Gly Glu Ser
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233      245          250          255
234      Lys Arg Asn Arg
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VERIFICATION SUMMARY
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